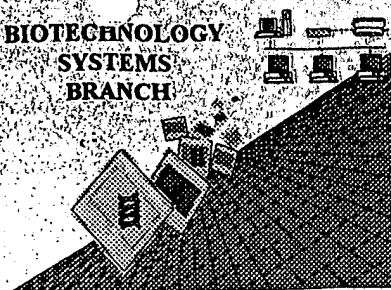


03/60

0880

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer-readable form:

Application Serial Number:

09/714,712

Source:

OIPF

Date Processed by STIC:

4/16/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/714,712

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 \_\_\_\_\_ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 \_\_\_\_\_ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 \_\_\_\_\_ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 \_\_\_\_\_ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 \_\_\_\_\_ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 \_\_\_\_\_ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 \_\_\_\_\_ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 \_\_\_\_\_ Skipped Sequences (OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 \_\_\_\_\_ Skipped Sequences (NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 \_\_\_\_\_ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 \_\_\_\_\_ Use of "Artificial" (NEW RULES)      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.
- 12 \_\_\_\_\_ Use of <220>Feature (NEW RULES)      Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 \_\_\_\_\_ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIEP

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/714,712

DATE: 04/16/2001  
 TIME: 17:28:44

Input Set : A:\PTO.txt  
 Output Set: N:\CRF3\04162001\I714712.raw

Does Not Comply  
 Corrected Diskette Needed

3 <110> APPLICANT: Schmitz, et al.  
 5 <120> TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS SPECIFIC FOR DENDRITIC CELLS COMPOSITIONS AND  
 6 METHODS OF USE THEREOF ANTIGENS RECOGNIZED THEREBY AND CELLS OBTAINED THEREBY  
 8 <130> FILE REFERENCE: 830003-2002.1  
 10 <140> CURRENT APPLICATION NUMBER: 09/714,712  
 11 <141> CURRENT FILING DATE: 2000-11-15  
 13 <150> PRIOR APPLICATION NUMBER: 60/165,555  
 14 <151> PRIOR FILING DATE: 1999-11-15  
 16 <160> NUMBER OF SEQ ID NOS: 38  
 18 <170> SOFTWARE: PatentIn version 3.0  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 1312  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Homo sapiens  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: misc\_feature  
 27 <222> LOCATION: (1)..(1312)  
 28 <223> OTHER INFORMATION: BDCA-2 cDNA sequence  
 31 <400> SEQUENCE: 1  
 32 cagtgaattct cgtgcctcag cctcctgagt agccgaaatt acagacgtgt gccaccatgc 60  
 34 ttggctaatt ttttggattt ttagtagaga tggggtttca ctatgttggc caggetagtc 120  
 36 ttgaactcct ggcctgaagc aatccgcccc cctcagcctc ccaaagtgcg gagattatag 180  
 38 gcacgagcca ctacacctgg ccacaaaatt ctttaaagaa gccaatccca tcctccctca 240  
 40 agagccaagg ggccacctca ccctcttggt acagcagatc ctgcctccac agtcaccctg 300  
 42 ctcccaagtg caacctctgt ctgacctgc atggtgtgog gtgcctcct gcctcaggcc 360  
 44 gcgaagaagg atctaagggc ttggtctggt tgaaagaacc acaccccgaa agtaacatct 420  
 46 ttggagaaag tgatacaaga gcttctgcac ccacctgata gaggaagtcc aaaggggtgtg 480  
 48 ogcacacaca atggtgcctg aagaagagcc tcaagaccga gagaaaggac tctggtggtt 540  
 50 ccagttgaag gtctggtoca tggcagtcgt atccatcttg ctccctcagt tctgtttcac 600  
 52 tgtgagttct gtggtgcctc acaattttat gtatagcaaa actgtcaaga ggctgtccaa 660  
 54 gttacgagag tatcaacagt atcatccaag cctgacctgc gtcattggaag gaaaggacat 720  
 56 agaagattgg agctgctgcc caaccccttg gacttcattt cagtctagtt gctactttat 780  
 58 ttctactggg atgcaatctt ggactaagag tcaaaagaac tgttctgtga tgggggctga 840  
 60 tctggtggtg atcaacacca ggaagaaca ggatttcac attcagaatc tgaaaagaaa 900  
 62 ttcttcttat tttctggggc tgtcagatcc agggggtcgg cgacattggc aatgggttga 960  
 64 ccagacacca tacaatgaaa atgtcacatt ctggcactca ggtgaaccca ataaccttga 1020  
 66 tgagcgttgt gcgataataa atttccgttc ttcagaagaa tggggctgga atgacattca 1080  
 68 ctgtcatgta cctcagaagt caatttgcaa gatgaagaag atctacatat aaatgaaata 1140  
 70 ttctccctgg aaatgtgttt ggggtggcat ccaccgttgt agaaagctaa attgattttt 1200  
 72 taattttatgt gtaagttttg tacaaggaat gcccttaaaa tgtttcagca ggctgtcacc 1260  
 74 tattacaact atgatataat ccaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1312  
 77 <210> SEQ ID NO: 2  
 78 <211> LENGTH: 213  
 79 <212> TYPE: PRT  
 80 <213> ORGANISM: Homo sapiens  
 82 <220> FEATURE:  
 83 <221> NAME/KEY: UNSURE

see  
 p. 5

## RAW SEQUENCE LISTING

DATE: 04/16/2001

PATENT APPLICATION: US/09/714,712

TIME: 17:28:44

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04162001\I714712.raw

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84 <222> LOCATION: (1)..(213)
85 <223> OTHER INFORMATION: amino acid sequence of one of the isoforms of BDCA-2 with all six
87     exons expressed
90 <400> SEQUENCE: 2
92 Met Val Pro Glu Glu Pro Gln Asp Arg Glu Lys Gly Leu Trp Trp
93 1           5           10           15
95 Phe Gln Leu Lys Val Trp Ser Met Ala Val Val Ser Ile Leu Leu Leu
96           20           25           30
98 Ser Val Cys Phe Thr Val Ser Ser Val Val Pro His Asn Phe Met Tyr
99           35           40           45
101 Ser Lys Lys Thr Val Lys Arg Leu Ser Lys Leu Arg Glu Tyr Gln Gln Tyr
102           50           55           60
104 His Pro Ser Leu Thr Cys Val Met Glu Gly Lys Asp Ile Glu Asp Trp
105 65           70           75           80
107 Ser Cys Cys Pro Thr Pro Trp Thr Ser Phe Gln Ser Ser Cys Tyr Phe
108           85           90           95
110 Ile Ser Thr Gly Met Gln Ser Trp Thr Lys Ser Gln Lys Asn Cys Ser
111           100          105          110
113 Val Met Gly Ala Asp Leu Val Val Ile Asn Thr Arg Glu Glu Gln Asp
114           115          120          125
116 Phe Ile Ile Gln Asn Leu Lys Arg Asn Ser Ser Tyr Phe Leu Gly Leu
117           130          135          140
119 Ser Asp Pro Gly Gly Arg His Trp Gln Trp Val Asp Gln Thr Pro
120 145          150          155          160
122 Tyr Asn Glu Asn Val Thr Phe Trp His Ser Gly Glu Pro Asn Asn Leu
123           165          170          175
125 Asp Glu Arg Cys Ala Ile Ile Asn Phe Arg Ser Ser Glu Glu Trp Gly
126           180          185          190
128 Trp Asn Asp Ile His Cys His Val Pro Gln Lys Ser Ile Cys Lys Met
129           195          200          205
131 Lys Lys Ile Tyr Ile
132           210
134 <210> SEQ ID NO: 3
135 <211> LENGTH: 1227
136 <212> TYPE: DNA
137 <213> ORGANISM: Mus musculus
139 <220> FEATURE:
140 <221> NAME/KEY: CDS
141 <222> LOCATION: (146)..(775)
142 <223> OTHER INFORMATION: coding sequence of mouse Dectin-2
145 <300> PUBLICATION INFORMATION:
146 <308> DATABASE ACCESSION NO: AF240357
147 <309> DATABASE ENTRY DATE: 2000-05-02
148 <313> RELEVANT RESIDUES: (1)..(1227)
150 <400> SEQUENCE: 3
151 cattggcccg ctctgtggca tttactcaa gtgtgtgtgg aagttgattc tgaactctgg      60
153 cctctttgac agaagccagg tccctgagtc gtattttgga gacagatgca agaaaccct      120
155 gaccttctga acatacacct caaca atg gtg cag gaa aga caa tcc caa ggg      172
156           Met Val Gln Glu Arg Gln Ser Gln Gly

```

## RAW SEQUENCE LISTING

DATE: 04/16/2001

PATENT APPLICATION: US/09/714,712

TIME: 17:28:44

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04162001\I714712.raw

```

157                                     1               5
159 aag gga gtc tgc tgg acc ctg aga ctc tgg tca gct gct gtg att tcc      220
160 Lys Gly Val Cys Trp Thr Leu Arg Leu Trp Ser Ala Ala Val Ile Ser
161 10                               15                20                25
163 atg tta ctc ttg agt acc tgt ttc att gcg agc tgt gtg gtg act tac      268
164 Met Leu Leu Leu Ser Thr Cys Phe Ile Ala Ser Cys Val Val Thr Tyr
165                               30                35                40
167 caa ttt att atg gac cag ccc agt aga aga cta tat gaa ctt cac aca      316
168 Gln Phe Ile Met Asp Gln Pro Ser Arg Arg Leu Tyr Glu Leu His Thr
169                               45                50                55
171 tac cat tcc agt ctc acc tgc ttc agt gaa ggg act atg gtg tca gaa      364
172 Tyr His Ser Ser Leu Thr Cys Phe Ser Glu Gly Thr Met Val Ser Glu
173                               60                65                70
175 aaa atg tgg gga tgc tgc cca aat cac tgg aag tca ttt ggc tcc agc      412
176 Lys Met Trp Gly Cys Cys Pro Asn His Trp Lys Ser Phe Gly Ser Ser
177                               75                80                85
179 tgc tac ctc att tct acc aag gag aac ttc tgg agc acc agt gag cag      460
180 Cys Tyr Leu Ile Ser Thr Lys Glu Asn Phe Trp Ser Thr Ser Glu Gln
181 90                               95                100                105
183 aac tgt gtt cag atg ggg gct cat ctg gtg gtg atc aat act gaa gcg      508
184 Asn Cys Val Gln Met Gly Ala His Leu Val Val Ile Asn Thr Glu Ala
185                               110                115                120
187 gag cag aat ttc atc acc cag cag ctg aat gag tca ctt tct tac ttc      556
188 Glu Gln Asn Phe Ile Thr Gln Gln Leu Asn Glu Ser Leu Ser Tyr Phe
189                               125                130                135
191 ctg ggt ctt tcg gat cca caa ggt aat ggc aaa tgg caa tgg atc gat      604
192 Leu Gly Leu Ser Asp Pro Gln Gly Asn Gly Lys Trp Gln Trp Ile Asp
193                               140                145                150
195 gat act cct ttc agt caa aat gtc agg ttc tgg cac ccc cat gaa ccc      652
196 Asp Thr Pro Phe Ser Gln Asn Val Arg Phe Trp His Pro His Glu Pro
197                               155                160                165
199 aat ctt cca gaa gag cgg tgt gtt tca ata gtt tac tgg aat cct tcg      700
200 Asn Leu Pro Glu Glu Arg Cys Val Ser Ile Val Tyr Trp Asn Pro Ser
201 170                               175                180                185
203 aaa tgg ggc tgg aat gat gtt ttc tgt gat agt aaa cac aat tca ata      748
204 Lys Trp Gly Trp Asn Asp Val Phe Cys Asp Ser Lys His Asn Ser Ile
205                               190                195                200
207 tgt gaa atg aag aag att tac cta tga gtgcctgtta ttcattaata      795
208 Cys Glu Met Lys Lys Ile Tyr Leu
209                               205
211 tcttttaaagt tcagacctac caagaagcca taacttcttg gcctgtacat ctgacagagg      855
213 cgtttctttt cctagccact attctttact caaacagaat gagccctttc tccttctgat      915
215 ggtagagtt ttgtcaactt gacacaaact agagtcacct ggggagtagg atcttcagct      975
217 aaggaattgc ctctgtcagc ttgaccagtc agcatgtctg ggggcatttt cttgattaat      1035
219 gattgttgta agagggtcca ggtggtgaagc aaagggtgta aaccatgaa gagcaagcca      1095
221 gggagcatca tccatccatc tctgccctca ggtttctgcc ccagggtctt gccctggttt      1155
223 ctttctatga actgctgtta cttgaaagta taagatgaat aaacaatttc atccaaaaaa      1215
225 aaaaaaaaaa aa                                1227
228 <210> SEQ ID NO: 4

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RAW SEQUENCE LISTING                      DATE: 04/16/2001  
 PATENT APPLICATION: US/09/714,712        TIME: 17:28:44

Input Set : A:\PTO.txt  
 Output Set: N:\CRF3\04162001\I714712.raw

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229 <211> LENGTH: 209
230 <212> TYPE: PRT
231 <213> ORGANISM: Mus musculus
233 <400> SEQUENCE: 4
235 Met Val Gln Glu Arg Gln Ser Gln Gly Lys Gly Val Cys Trp Thr Leu
236 1          5          10          15
239 Arg Leu Trp Ser Ala Ala Val Ile Ser Met Leu Leu Leu Ser Thr Cys
240          20          25          30
243 Phe Ile Ala Ser Cys Val Val Thr Tyr Gln Phe Ile Met Asp Gln Pro
244          35          40          45
247 Ser Arg Arg Leu Tyr Glu Leu His Thr Tyr His Ser Ser Leu Thr Cys
248          50          55          60
251 Phe Ser Glu Gly Thr Met Val Ser Glu Lys Met Trp Gly Cys Cys Pro
252 65          70          75          80
255 Asn His Trp Lys Ser Phe Gly Ser Ser Cys Tyr Leu Ile Ser Thr Lys
256          85          90          95
259 Glu Asn Phe Trp Ser Thr Ser Glu Gln Asn Cys Val Gln Met Gly Ala
260          100         105         110
263 His Leu Val Val Ile Asn Thr Glu Ala Glu Gln Asn Phe Ile Thr Gln
264          115         120         125
267 Gln Leu Asn Glu Ser Leu Ser Tyr Phe Leu Gly Leu Ser Asp Pro Gln
268          130         135         140
271 Gly Asn Gly Lys Trp Gln Trp Ile Asp Asp Thr Pro Phe Ser Gln Asn
272 145         150         155         160
275 Val Arg Phe Trp His Pro His Glu Pro Asn Leu Pro Glu Glu Arg Cys
276          165         170         175
279 Val Ser Ile Val Tyr Trp Asn Pro Ser Lys Trp Gly Trp Asn Asp Val
280          180         185         190
283 Phe Cys Asp Ser Lys His Asn Ser Ile Cys Glu Met Lys Lys Ile Tyr
284          195         200         205
287 Leu
291 <210> SEQ ID NO: 5
292 <211> LENGTH: 237
293 <212> TYPE: PRT
294 <213> ORGANISM: Homo sapiens
296 <220> FEATURE:
297 <221> NAME/KEY: UNSURE
298 <222> LOCATION: (1)..(237)
299 <223> OTHER INFORMATION: amino acid sequence of human DCIR
302 <300> PUBLICATION INFORMATION:
303 <308> DATABASE ACCESSION NO: AJ133532
304 <309> DATABASE ENTRY DATE: 1999-09-01
305 <313> RELEVANT RESIDUES: (1)..(237)
307 <400> SEQUENCE: 5
309 Met Thr Ser Glu Ile Thr Tyr Ala Glu Val Arg Phe Lys Asn Glu Phe
310 1          5          10          15
312 Lys Ser Ser Gly Ile Asn Thr Ala Ser Ser Ala Ala Ser Lys Glu Arg
313          20          25          30
315 Thr Ala Pro His Lys Ser Asn Thr Gly Phe Pro Lys Leu Leu Cys Ala

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/714,712

DATE: 04/16/2001

TIME: 17:28:44

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04162001\I714712.raw

```

316          35          40          45
318 Ser Leu Leu Ile Phe Phe Leu Leu Ala Ile Ser Phe Phe Ile Ala
319          50          55          60
321 Phe Val Ile Phe Phe Gln Lys Tyr Ser Gln Leu Leu Glu Lys Lys Thr
322 65          70          75          80
324 Thr Lys Glu Leu Val His Thr Thr Leu Glu Cys Val Lys Lys Asn Met
325          85          90          95
327 Pro Val Glu Glu Thr Ala Trp Ser Cys Cys Pro Lys Asn Trp Lys Ser
328          100          105          110
330 Phe Ser Ser Asn Cys Tyr Phe Ile Ser Thr Glu Ser Ala Ser Trp Gln
331          115          120          125
333 Asp Ser Glu Lys Asp Cys Ala Arg Met Glu Ala His Leu Leu Val Ile
334          130          135          140
336 Asn Thr Gln Glu Glu Gln Asp Phe Ile Phe Gln Asn Leu Gln Glu Glu
337 145          150          155          160
339 Ser Ala Tyr Phe Val Gly Leu Ser Asp Pro Glu Gly Gln Arg His Trp
340          165          170          175
342 Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Ser Ser Thr Phe Trp His
343          180          185          190
345 Pro Arg Glu Pro Ser Asp Pro Asn Glu Arg Cys Val Val Leu Asn Phe
346          195          200          205
348 Arg Lys Ser Pro Lys Arg Trp Gly Trp Asn Asp Val Asn Cys Leu Gly
349          210          215          220
351 Pro Gln Arg Ser Val Cys Glu Met Met Lys Ile His Leu
352 225          230          235

```

354 <210> SEQ ID NO: 6  
 355 <211> LENGTH: 5  
 356 <212> TYPE: PRT  
 C--> 357 <213> ORGANISM: Artificial *see item 11 on Ena Summary Sheet*  
 359 <220> FEATURE:  
 360 <223> OTHER INFORMATION: basic unit of a linking peptide  
 362 <400> SEQUENCE: 6  
 364 Gly Gly Gly Gly Ser  
 365 1 5  
 367 <210> SEQ ID NO: 7  
 368 <211> LENGTH: 24  
 369 <212> TYPE: DNA  
 C--> 370 <213> ORGANISM: Artificial  
 372 <220> FEATURE:  
 373 <223> OTHER INFORMATION: primer  
 375 <400> SEQUENCE: 7  
 376 ttgaaagaac cacaccccgga aagt  
 379 <210> SEQ ID NO: 8  
 380 <211> LENGTH: 24  
 381 <212> TYPE: DNA  
 C--> 382 <213> ORGANISM: Artificial  
 384 <220> FEATURE:  
 385 <223> OTHER INFORMATION: primer  
 387 <400> SEQUENCE: 8

24

**Please Note:**

Use f n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/714,712

DATE: 04/16/2001

TIME: 17:28:45

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04162001\I714712.raw

L:357 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:370 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:382 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37